

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANTS: Graves, Scott S.  
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(ii) TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT BIND TO THE  
ANTIGEN BOUND BY ANTIBODY NR-LU-13 AND THEIR USE IN  
PRETARGETING METHODS

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US  
(B) FILING DATE: 24-JAN-2002  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 690022.527C2

(ix) TELECOMMUNICATION INFORMATION:

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## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCTGACGAAT TCGTTGACAT TGATTATTGA C

31

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCTGACGCGG CCGCTTCGAT AAGCCAGTAA GC

32

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTTCGGCTCG AGCACAGCTA GCATTATCTG GGATAAGCAT GCTG

44

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTТАСGGGGC CCCTAACACT CTCCCCTGTT GAAG

34

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTACGCGGAT CCCAGACACT GGACGCTG

28

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CATTCGGAAT TCGAACCATC ACAGTCTCGC

30

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCTGACGAAT TCTCATTAC CCGGAGACAG GGAG

34

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGTCTATTA CTGTTCTAGA GAGGTC

26

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAGCGTGC GG CCGCACCATG GACATCAGGG CTCCTGCTCA G

41

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGCAGTACCA AAGCACGTAC CGGGTG

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TACGTGCTTT GGTACTGCTC CTC

23

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCTGACGGAT CCTCATTTAC CCGGAGACAG GGAG

34

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCGTCTATT A CTGTTCTAGA GAGGTC

26

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 360 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAG GTT CAG CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG CCA GGG GCC  
 Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala  
 1 5 10 15

48

TCA GTC AGG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT AAA GAC ACC  
 Ser Val Arg Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr  
 20 25 30

96

TAT ATG CAC TGG GTG ATA GAG AGG CCT GAA CAG GGC CTG GAG TGG ATT  
 Tyr Met His Trp Val Ile Glu Arg Pro Glu Gln Gly Leu Glu Trp Ile  
 35 40 45

144

GGA AGG ATT GAT CCT GCG AAT GGT AAT ACT AAA TGT GAC CCG AAG TTC Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Cys Asp Pro Lys Phe	192
50 55 60	
CAG GGC AAG GCC ACT ATA ACA GCA GAC ACA TCC TCC AAC ACA GCC TAC Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr	240
65 70 75 80	
CTG CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC TAT TAC TGT Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys	288
85 90 95	
TCT AGA GAG GTC CTA ACT GGG ACG TGG TCT TTG GAC TAC TGG GGT CAA Ser Arg Glu Val Leu Thr Gly Thr Trp Ser Leu Asp Tyr Trp Gly Gln	336
100 105 110	
GGA ACC TCA GTC ACC GTC TCC TCA Gly Thr Ser Val Thr Val Ser Ser	360
115 120	

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 120 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala	
1 5 10 15	
Ser Val Arg Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr	
20 25 30	
Tyr Met His Trp Val Ile Glu Arg Pro Glu Gln Gly Leu Glu Trp Ile	
35 40 45	
Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Cys Asp Pro Lys Phe	
50 55 60	
Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr	
65 70 75 80	
Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
Ser Arg Glu Val Leu Thr Gly Thr Trp Ser Leu Asp Tyr Trp Gly Gln	
100 105 110	
Gly Thr Ser Val Thr Val Ser Ser	
115 120	

## (2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..321

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAC ATC CAG ATG ATT CAG TCT CCA TCG TCC ATG TTT GCC TCT CTG GGA Asp Ile Gln Met Ile Gln Ser Pro Ser Ser Met Phe Ala Ser Leu Gly	48
1 5 10 15	
GAC AGA GTC AGT CTC TCT TGT CGG GCT AGT CAG GGC ATT AGA GGT AAT Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Gly Ile Arg Gly Asn	96
20 25 30	
TTA GAC TGG TAT CAG CAG AAA CCA GGT GGA ACT ATT AAA CTC CTG ATC Leu Asp Trp Tyr Gln Gln Lys Pro Gly Gly Thr Ile Lys Leu Leu Ile	144
35 40 45	
TAC TCC ACA TCC AAT TTA AAT TCT GGT GTC CCA TCA AGG TTC AGT GGC Tyr Ser Thr Ser Asn Leu Asn Ser Gly Val Pro Ser Arg Phe Ser Gly	192
50 55 60	
AGT GGG TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC AGC CTA GAC TCT Ser Gly Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Asp Ser	240
65 70 75 80	
GAA GAT TTT GCA GAC TAT TAC TGT CTA CAG CGT AAT GCG TAT CCG TAC Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Arg Asn Ala Tyr Pro Tyr	288
85 90 95	
ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys	321
100 105	

## (2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Asp Ile Gln Met Ile Gln Ser Pro Ser Ser Met Phe Ala Ser Leu Gly  
 1 5 10 15

Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Gly Ile Arg Gly Asn  
 20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Gly Thr Ile Lys Leu Leu Ile  
 35 40 45

Tyr Ser Thr Ser Asn Leu Asn Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60

Ser Gly Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Asp Ser  
 65 70 75 80

Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Arg Asn Ala Tyr Pro Tyr  
 85 90 95

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys  
 100 105

## (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 107 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Gly Asn  
 20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Gly Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ser Thr Ser Asn Leu Asn Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60

Ser Gly Ser Gly Ser Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Arg Asn Ala Tyr Pro Tyr  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
 100 105

## (2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Thr  
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Gln Trp Met  
35 40 45

Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Cys Asp Leu Ser Phe  
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Ile Asn Thr Ala Tyr  
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ser Arg Glu Val Leu Thr Gly Thr Trp Ser Leu Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
115 120